

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Beach, David H.
Demetrick, Douglas J.
Serrano, Manuel
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(ii) TITLE OF INVENTION: Antibodies to Cell-Cycle Regulatory Proteins, and
Uses Related Thereto

(iii) NUMBER OF SEQUENCES: 34

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPad

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/016,869
(B) FILING DATE: 30-JAN-1998

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 15-JUL-1994

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 14-SEP-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/248,812
(B) FILING DATE: 25-MAY-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/227,371
(B) FILING DATE: 14-APR-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/154,915
(B) FILING DATE: 18-NOV-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/991,997
(B) FILING DATE: 17-DEC-1992

(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG
 Met Asp Pro Ala Ala 5
 1
 GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCG
 Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala
 10 15 20 103
 CGG GGT CGG GTA GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG
 Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu
 25 30 35 151
 CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG
 Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met
 40 45 50 199
 ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG
 Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu
 55 60 65 247
 CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT
 Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala
 70 75 80 85 295
 GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG
 Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly
 90 95 100 343
 GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG
 Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu
 105 110 115 391
 GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT
 Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
 120 125 130 439
 GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA
 Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu
 135 140 145 487
 GGT CCC TCA GAC ATC CCC GAT TGAAAGAACCC AGAGAGGCTC TGAGAACCT
 Gly Pro Ser Asp Ile Pro Asp 538

150	155					
CGGGAAACTT	AGATCATCAG	TCACCGAAGG	TCCTACAGGG	CCACAACTGC	CCCCGCCACA	598
ACCCACCCCG	CTTCTGTAGT	TTTCATTTAG	AAAATAGAGC	TTTTAAAAAT	GTCCTGCCTT	658
TTAACGTAGA	TATAAGCCTT	CCCCCACTAC	CGTAAATGTC	CATTTATATC	ATTTTTATA	718
TATTCTTATA	AAAATGTAAA	AAAGAAAAAC	ACCGCTTCTG	CCTTTTCACT	GTGTTGGAGT	778
TTTCTGGAGT	GAGCACTCAC	GCCCTAAGCG	CACATTATG	TGGGCATTTC	TTGCGAGCCT	838
CGCAGCCTCC	GGAAGCTGTC	GACTTCATGA	CAAGCATTT	GTGAACTAGG	GAAGCTCAGG	898
GGGGTTACTG	GCTTCTCTTG	AGTCACACTG	CTAGCAAATG	GCAGAACCAA	AGCTCAAATA	958
AAAATAAAAT	TATTTTCATT	CATTCACTCA	AAAAAA			994

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Pro	Ala	Ala	Gly	Ser	Ser	Met	Glu	Pro	Ser	Ala	Asp	Trp	Leu	
1					5				10					15		
Ala	Thr	Ala	Ala	Ala	Arg	Gly	Arg	Val	Glu	Glu	Val	Arg	Ala	Leu	Leu	
					20				25					30		
Glu	Ala	Val	Ala	Leu	Pro	Asn	Ala	Pro	Asn	Ser	Tyr	Gly	Arg	Arg	Pro	
					35				40					45		
Ile	Gln	Val	Met	Met	Gly	Ser	Ala	Arg	Val	Ala	Glu	Leu	Leu	Leu		
					50				55					60		
Leu	His	Gly	Ala	Glu	Pro	Asn	Cys	Ala	Asp	Pro	Ala	Thr	Leu	Thr	Arg	
					65				70					75		80
Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val	Val	
					85				90					95		
Leu	His	Arg	Ala	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly	Arg	
					100				105					110		
Leu	Pro	Val	Asp	Leu	Ala	Glu	Glu	Leu	Gly	His	Arg	Asp	Val	Ala	Arg	
					115				120					125		
Tyr	Leu	Arg	Ala	Ala	Ala	Gly	Gly	Thr	Arg	Gly	Ser	Asn	His	Ala	Arg	
					130				135					140		
Ile	Asp	Ala	Ala	Glu	Gly	Pro	Ser	Asp	Ile	Pro	Asp					
					145				150					155		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG 60
CGCTAGGCGC TTTTCCCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA 120
AAAGCCCGGA GCTAACGACC GGCGCCTCGG CACTGCACGG GGCCCCAAGC CGCAGAAGAA 180
GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTCGCCGG 240
AGCAGCGTGG GAAAAGAAGGG AAGAGTGTCTG TTAAGTTAC GGCCAACGGT GGATTATCCG 300
GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG AAC AAG GGC ATG 351
Met Arg Glu Glu Asn Lys Gly Met
1 5
CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA 399
Pro Ser Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
10 15 20
CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC 447
Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn
25 30 35 40
GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC 495
Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly
45 50 55
AGC GCC CGC GTG GCG GAG CTG CTG CTC CAC GGC GCG GAG CCC AAC 543
Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn
60 65 70
TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG 591
Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg
75 80 85
GAG GGC TTC CTG GAC ACG CTG GTG CTG CTG CAC CGG GCC GGG GCG CGG 639
Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
90 95 100
CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG 687
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu
105 110 115 120
GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG 735
Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly
125 130 135
GAC TGACGCCAGG TTCCCCAGCC GCCCACAAACG ACTTTATTTT CTTACCCAAT 788
Asp
TTCCCCACCCCC CACCCACCTA ATTGATGAA GGCTGCCAAC GGGGAGCGG 837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Ser Asp Glu
1 5 10 15
Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
20 25 30
Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
35 40 45
Ala Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu
50 55 60
Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr

65	70	75		80
Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val				
	85	90		95
Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly				
	100	105		110
Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala				
	115	120		125
Gly Tyr Leu Arg Thr Ala Thr Gly Asp				
	130	135		

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 853 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - ii) MOLECULE TYPE: cDNA
 - ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 213..587
 - xi) SEQUENCE DESCRIPTION: SEQ I

Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp
90 95 100

GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT CGC GGC 569
Gly His Ser Phe Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly
105 110 115

CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCCGCC TTTTCTTCT 617
Gln Ser Gln Glu Gln Ser
120 125

TAGCTTCACT TCTAGCGATG CTAGCGTGTC TAGCATGTGG CTTTAAAAAA TACATAATAA 677

TGCTTTTTT GCAATCACGG GAGGGAGCAG AGGGAGGGAG CAGAAGGAGG GAGGGAGGGA 737

GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAAACTG AGCGAAGGCG GCCGCGAAGG 797

GAATAATGGC TGGATTGTTT AAAAAATAA AATAAAGATA CTTTTAAAAA TGTCAA 853

(2) INFORMATION FOR SEQ ID NO:6:

- Q7
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly
1 5 10 15

Ala Asp Ser Asn Cys Gly Asp Pro Thr Thr Phe Ser Arg Pro Val His
20 25 30

Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly
35 40 45

Ser Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu
50 55 60

Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg
65 70 75 80

Ser Ala Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys Thr Ala
85 90 95

Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser Thr Pro
100 105 110

Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCA CTC CTG GAA GCC GGC GCA GAT CCC AAC GCC CTG AAC CGC TTC GGG 48
Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
1 5 10 15
AGG CGC CCA ATC CAG GTC ATG ATG GGC AGC GCC AGG GTG GCA GAG 96
Arg Arg Pro Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu
20 25 30
CTG CTG CTG CTC CAC GGA GCA GAA CCC AAC TGC GCC GAC CCT GCC ACC 144
Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
35 40 45
CTT ACC AGA CCT GTG CAC GAC GCA GCT CGG GAA GGC TTC CTG GAC ACG 192
Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Phe Leu Asp Thr
50 55 60
CTT GTC GTG CTG CAC CGG GCA GGG GCG CGG TTG GAT GTG 231
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
1 5 10 15
Arg Arg Pro Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu
20 25 30
Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
35 40 45
Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Phe Leu Asp Thr
50 55 60
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15
Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
20 25 30
Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly
35 40 45 50 55 60
Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
65 70 75 80
Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
85 90 95
Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
100 105 110
Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
115 120 125
Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
130 135 140
Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
145 150 155 160
Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
165 170 175
Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
180 185 190
Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
195 200 205
Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
210 215 220
Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg
225 230 235 240

Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro
245 250 255
Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu
260 265 270
Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg
275 280 285
Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu
290 295 300

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Lys Asp Gly Leu Cys Arg Ala Asp Gln Gln Tyr Glu Cys Val
1 5 10 15
Ala Glu Ile Gly Glu Gly Ala Tyr Gly Lys Val Phe Lys Ala Xaa Asp
20 25 30
Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln
35 40 45
Thr Gly Glu Glu Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val
50 55 60
Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe
65 70 75 80
Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu
85 90 95
Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val
100 105 110
Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln
115 120 125
Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg
130 135 140
Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys
145 150 155 160

Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu
165 170 175

Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu
180 185 190

Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile
195 200 205

Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp
210 215 220

Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu
225 230 235 240

Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser
245 250 255

Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu
260 265 270

Gly Lys Asp Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg
275 280 285

Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu
290 295 300

Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr
305 310 315 320

Ser Glu Leu Asn Thr Ala
325

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
35 40 45

Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
50 55 60

Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65 70 75 80

Arg Xaa Ala Xaa Gly
85

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
20 25 30

Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45

Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu
50 55 60

Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa
65 70 75 80

Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
85 90 95

Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
100 105 110

Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa
115 120 125

Xaa Tyr Leu Arg Xaa Ala Xaa Gly Gly Thr Arg Gly Ser Asn His Ala
130 135 140

Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp

145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

D/
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Ser Asp Glu
1 5 10 15
Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
20 25 30
Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
35 40 45
Ala Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu
50 55 60
Leu Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa
65 70 75 80
Xaa Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu
85 90 95
Val Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp
100 105 110
Gly Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa
115 120 125
Xaa Xaa Tyr Leu Arg Xaa Ala Xaa Gly Asp
130 135

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1 5 10 15

Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
35 40 45

Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
50 55 60

Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65 70 75 80

Arg Xaa Ala Xaa Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys
85 90 95

Thr Ala Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser
100 105 110

Thr Pro Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Ala Glu Ile Gly Xaa Gly Ala Tyr Gly Xaa Val Xaa Lys Ala Arg Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Xaa Lys Ala Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- Q/1
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ala Arg Asp
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 960 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAGAGGGGA ATT CGGCACGA GGCAGCATG GAGCCTTCGG CTGACTGGCT GGCCACGGCC	60
GCGGCCGGG GTCGGTAGA GGAGGTGCGG GCGCTGCTGG AGGCGGTGGC GCTGCCCAA	120
CGCACCGAAT AGTTACGGTC GGAGGCCGAT CCAGGTATG GATGATGGGC AGCGCCCCGA	180
GTGGCGGAGC TGCTGCTGCT CCACGGCGCG GAGCCAACT GCGCCGACCC CGCCACTCTC	240
ACCCGACCCG TGCACCACGC TGCCCGGGAG GGCTTCTGGA CACGCTGGTG GTGCTGCACC	300
GGGCCGGGGC GCGGCTGGAC GTGCGCGATG CCTGGGGCCG TCTGCCGTG GACCTGGCTG	360
AGGAGCTGGG CCATCGCGAT GTCGCACGGT ACCTGCGCGC CCGTGCAGGG GGCACCAAGAG	420

GCAGTAACCA TGCCCGATA GATGCCGCGG AAGGTCCCTC AGACATCCCC	480
ACCAGAGAGG CTCTGAGAAA CCTCGGGAAA CTTAGATCAT CAGTCACCGA AGGTCCCTACA	540
GGGCCACAAAC TGCCCCCGCC ACAACCCACC CCGCTTCGT AGTTTCATT TAGAAAATAG	600
AGCTTTAAA AATGTCCTGC CTTTAACGT AGATATAAGC CTTCCCCCAC TACCGTAAAT	660
GTCCATTTAT ATCATTTTTT ATATATTCTT ATAAAAATGT AAAAAAAGAA AAACACCGCT	720
TCTGCCTTT CACTGTGTTG GAGTTTCTG GAGTGAGCAC TCACGCCCTA AGCGCACATT	780
CATGTGGGCA TTTCTTGCAGC GCCTCGCAGC CTCCGGAAGC TGTCGACTTC ATGACAAGCA	840
TTTTGTGAAC TAGGGAAAGCT CAGGGGGGTT ACTGGCTTCT CTTGAGTCAC ACTGCTAGCA	900
AATGGCAGAA CCAAAGCTCA AATAAAAATA AAATTATTTT CATTCAATTCA CTCAAAAAAA	960

(2) INFORMATION FOR SEQ ID NO:19:

- D7
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGNGGNAAGN TGTGGGGAA AGTTTGGGA TGGAANACCA ANCCCTCCTT TCNTTACCAA	60
ACNCTGGCTC TGNCGAGGCT NCNTCCGANT GGTNCCCCG GGGGAGACCC AACCTGGGN	120
GACTTCAGGG NTGCNACATT CATTCACTAA GTGCTNGGAG NTAATANCAC CTCCTCCGAG	180
CANNGACAGG NTCGGAGGGG GCTCTTCCCC CANCACCGGA GGAAGAAAGA GGAGGGNCTN	240
CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATGGATCCGG CGGGGGGGAG	300
CAGCATGGAN CCTTCGACTG ACTGACTGCC TCGC	334

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCNCTTATTG NTAGGANATA ATAACACCTC CACCGATAAC TTCACTTACA AGTCCCNNT	60
TCCTGGAAAG ATACACAGCG TTCCCTCCAG AGGATTGTG GGACAGGGTN GGAGNGGTCT	120
CTTCCNCCAC CACCGGAGGA AGAAAGAGGA GGGGCTGNCT GTTCACCGAGA GGGTGGGACG	180
GACCNCGTAC GCTCGNCNC TNCGGAGAGG GGGAGAGCAT CANCGNCGN CGGGGAGCAA	240
CATGGAACCG NCGGCGGGGA GCAGCATGGA NCCTCGGCT GACTGGCTGN CCACGNCCAC	300
GNCCCGGGGT CGGGTAGAGG AGGTGCAGNC GCTNCTGGAG CGGGGNCTC TGNCCAACNC	360
GCTAAAAN	368

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 404 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACNNNCTCC GGCGGGNGTC GGGTAGAGGA GGTGCAGGGCG CTGCTGGAGG CGGGGGCGCT	60
GCCCAACGCA CCGAATAGTT ACGGTGGAG GCCGATCCAG GTNNNGGTAG AGGGTCTGCA	120
GCGGGAGCAG GGGATGGCGG GCGACTCTGG AGGACGAAGT TTGCAGGGGA ATTGGAATCA	180
GGTAGCGCTT CGATTCTCCN GAAAAAGGGG AGGCTTCCTG GGGAGTTTC AGAAGGGTT	240
TGTAATCACA GACCTCCCTCC TGGCGACGTC CTGGGGGCTT GGGAAAGCAA GGAAGAGGAA	300
TNAGGAGCCA CGCGCGTACG AGTCTCTCGA ATGCTGAGAA GATCTNAAGG GGGAAACATA	360
TTTGTATTAG CNTCCAAGTN TNCTCTNTAT CANATACAAA NTNC	404

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCTNANCCC GGGTAGAGGG TCTGCAGCGG GAGCAGNGGA TGGCGGGCGA CTCTGGAGGA 60
CGAAGTTGGC AGGGGAATTG GAATCAGGTA GCGCTTCGAN TCTCCGGAAA AAGGGGAGGC 120
TTCCTGGGA GTTNNCAGAA GGGGTTTGTA ATCACAGNCC TCCNCCTGGC GACGCCCTGG 180
GGGGTTGGGA AGCCAAGGAA GAGGAATGAG GAGNCACGCG CNTACAGNTC TCTCGAATNC 240
TGANAAGATC TGAAGGGGG AACATATTG TATTAGNATN NAAGTATGCT CTTTATCAGA 300
TAGAAAATTC ACGAACGTGT GGNATAAAAA GGGAGTCTTA AAGAAATNTA AGATGTGCTG 360
GGACTACTTA GCCTCCAANA CACAGATNCC TGGATGGAGC T 401

37
(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAAANNAAAA AAAATCTCCC AGGCCTAACAA TAATTNTCAAG GAAAGAAATT TCAGTAGTTG 60
NATCTCAGGG GAAATACAGG AAGTTAGCCT GGAGTAAAAG TCAGTGTGTC CCTGCCCTT 120
TGCTANATTG CCCGTGCCTC ACAGTGCTCT CTGCTGTGA CGACAGCTCC NCAGAAGTTC 180
GGAGGATATA ATGGAATTCA TTGTGTACTG AAGAATGGAT AGAGAACTCA AGAAGGAAAT 240
TGGAAACTGG AAGCAAATGT AGGGGTAATT AGACACCTGG GGCTTCTGTG GGGGTCTGCT 300
TGGCGGTGAG GGGGCTCTAC ACAAGCTTCC TTTCCGTCAAT GCCGNCCCCC ACCCTGGCTC 360
TGACCATTCT GTTCTCTCTG GCAGGTCATG ATGATGGCA GCGCCCGAGG CGCGGAGCTG 420
CTGCTGCTCC ACGGCGCGGA GCCCACTGCT CCGACGCCG 459

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AANAAAAAAAG AAATNGATAA NATAGAGGAA TGAACANATT AAAATCAAAA AACANAACAN 60
AGACATAATA AAAAACGAGA ATGTTCTAGA CNTAACATCATA ATTATAAAGC TCAAGACTCA 120
TTGATATNAA GGADATTGAA GGGAAATCTT AACTAGCACA ANNGNATNAA AAAANAATTC 180
CCACGACACC GCCACTCTCA ACGCATCCGT GCTCGACACT GCCCGGGAGG TCNTCCTGGA 240
CACGCTGGTG GTNCTCCACC GGNCCGGGGC ACGTCTGGAC GTGCGCGATG CCTGGGNCCG 300
NCTACCCGTG GTACCTGACT GAGGACCTGG GCCATCCCAGA TTTGCNGGG TANCTCNNGN 360
GGCTGNNGGG GCCAANAGAG GNCANTACCC 390

① 1
(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGCNACGA CCCCCGCCACT CTCACCCGAC CCGTGCACGA CGCTGTCCGG GAGGGTTTCC 60
TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGNGCGGTT GGACGTGCGC GATGCCTGGG 120
GCCGCCTNCC CGTGNACCT GGTTGAGGAG CTGGGNACATC GCGATGTCGC ACGGTACCTG 180
CGCGCGTTGC GGGGGGCACC AGAGGNNAGT NACC 214

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

NCTCTCACGG TGGGGAGGCC AACTGCGCCG AACCCGCCAC TCTCACCCGA CCCCGGCACG	60
ACGGTGCCCC GGAGGGGTTTC CTGGACACGC TGGTGGTGCT GCACCGGGCC GGGCGCGGC	120
TGGACGTTCG NGATGCCTGG GGGNTCTNTC CGTNGNACCT GGCTGAAGAG CTGGNNCATC	180
GNGATGTCGC ACGGCCNCTG TGTGNGGNTG CGGGGGCAC CATAGTCAG TNTCC	235

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NAAGTATGAG CGAACNAAT TGTGGTTGA GAANAGGNAA TCGTAGGGAA CTTCGGGATC	60
CCNCNGGGAN CNCCAGAACCC TGAGNCGCCN ATTGGAAATN ACAAACTGNC TGNATCACTC	120
CGNACCAGGT NCAAAAGATA CCTGGGGANG CGGGAAGGGA AAGACNACAT CNAGACCGCC	180
TTCGCNCTN GGNATTGTGA GCAGCCTCTG AGACTCATTN ATATNACACT CTCGTNTTTC	240
TTCTTACAAC CCTGCGGNCC GOGCGGTGCG GCTTTCTCTG CCCTCCGCCG GGTGGACCTG	300
GAGCGCTTGA GCGGTCGGCG CGCCTGGAGC AGCCAGGCGG NCAGTGGACT AGCTGCTGGA	360
CCAGGGAGGT GTGGGAGAGC GGTGGCGGCG GGTACATGCA CGTGAAGCCA TTGCGAGAAC	420
TTTATCCATA AGTATTCAA TACCGTAGG GACGGCAAGA GAGGAGGGCG GGATGTGCCA	480
CACATCTTG ACCTCAGGTT TCTAACGCCT GTTTCTTTC TGCCCTCTGC AGACAACCCC	540
CGATTGAAAG AACCAAGAGAG GCTCTGAGAA ACC	573

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCCCATCGCG CCTTGGGANT GTGAGCNACC ATTGAGACTC ATNAATATAG CACTCGTTT	60
TCTTCTTGCA ACCCTGCCCN CGCGCGGTC GCGCTNTCTC TGCCCTCCGC NGGGTGGACC	120
TGGAGCGAGC GCTTGAGCGG TCGGTGGCG CNCCTGGANC AGCCAGGCGG GCAGTGGACT	180
ACCTNCTGGA CCAGGGACCT GTGGGAGAGC GGTGNCGCG GGTACATGCA CGTGAAGCCA	240
TTGCGAGAAC TTTATCCATA AGTATTTCAA TGCCGGTAGG GACGGCAAGA GAGGAGGGCG	300
GGATGTNCCA CACATCTTG ACCTCAGGTT TCTAACGCCT GTTTCTTTC TGCCCTCTGC	360
AGACATCCCC GATTGAAAGA ACCAGAGAGG CTCTGAGAAA CCTCCGGAAA CTTAGNTCAT	420
CANTCGCCGN AAAAA	434

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGAAATTAGA TCATCAGTCA CCGATCCTCC TACAGGGNCA CAACTGNCCC CGCCACAACC	60
CACCCCGNTT TCGTAGTTTT CATTAGAAA ATAGAGCTTT TAAAAATGTC CTGCCTTTA	120
ACGTAGATAT ATGCCTTCCC CCACTACCGN AAATGTCCAT TTATATCATN TTTTATATAT	180
TCTTATAAAA ATGTAAAAAA GAAAAACACC GCTTCTGCCT TTTCACTGTG TTGGAGTTTT	240
CTGGAGTGAG CACTCACGCC CTAAGCGCAC ATTCACTGTGG GCATTTCTTG CGAGCCTCGC	300
AGNCTCCGGA AGCTGTCGAC CTCGAGGGGG GGNCCGGTAC CCAATTGCC CTATACTGAG	360
TCGTATTACA ATTCACTGGN CGNCGNTTTT ACAACGTCGG TGGACTGGGA AAACCCCGGN	420
GTTACCCAAC TTTAATCGNC TTGGAGGACA TCCCCCTTT CGCCAGNTGG GGTTATAGNG	480
AAGAGGGCCN CACCNNTCGC CC	502

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

①
CANCNATNTN CGGCATTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTCG ACCTCGAGGG 60
GGGGNCCNGT ACCCAATTCTG NCCTATNGTG AGTCGTNTTA CAATTCACTG GCCGCCGTTT 120
TNACAAACGTC GNTGNACTGG GAAAACCCTG GTGTTACCCA ACTTNAATGT CCTTGNAGNA 180
CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA 240
ACAGTTGNNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTTT GTTAAAATTC 300
GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT 360
CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGAAACA 420
NGAGTCCACT ATTAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTCAGN 480
GGATTGGNCC ACTACGCNTA NCC 503

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CANCNATNTN CGGCATTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTCG ACCTCGAGGG 60
GGGGNCCNGT ACCCAATTCTG NCCTATNGTG AGTCGTNTTA CAATTCACTG GCCGCCGTTT 120
TNACAAACGTC GNTGNACTGG GAAAACCCTG GTGTTACCCA ACTTNAATCG CCTTGNAGNA 180
CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA 240
ACAGTTGNNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTTT GTTAAAATTC 300
GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT 360
CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGAAACA 420

NGAGTCCACT ATAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTCAGN
GGATTGGNCC ACTACGCNTA NCCATCACCC TATTG

480

515

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
1 5 10 15

His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30

His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50

Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
55 60 65

Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
70 75 80 85

Ala Gly Gly Thr

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu

1 5 10 15
His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
20 25 30
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
35 40 45 50
Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp/
55 60 65
Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala
70 75 80 85
Ala Gly Asp

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